

# Microbial Genomics & Bioprocessing Research

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## Research

### **Molecular Evolutionary Biology of *Fusarium***

Research in my laboratory focuses on several aspects of the evolutionary biology of *Fusarium*, a large genus of filamentous fungi that represents the single most important group of mycotoxigenic plant pathogens. *Fusaria* have also emerged within the past two decades as opportunistic and often fatal pathogens of severely immuno-compromised patients. Members of this genus produce an amazing diversity of toxic secondary metabolites, such as trichothecenes (potent inhibitors of eukaryotic protein synthesis and virulence-associated factors towards sensitive plant hosts), fumonisins (suspected carcinogens) and estrogenic compounds, which pose a serious threat to human and plant health and food safety. One of the primary goals of my research program is to develop molecular epidemiological tools for the rapid detection and identification of the most important fusarial pathogens of plants and humans. To achieve this objective, we have been using multilocus sequence typing (MLST) to identify species limits and to examine their population biology. Knowledge of species limits are essential for understanding their geographic distribution, host range and toxin potential. This information is critical in order to establish successful molecular surveillance programs for economically devastating plant diseases such as *Fusarium* Head Blight (FHB) of wheat and barley and Sudden Death Syndrome (SDS) of soybean (for publications, see below). Just within the past decade, FHB endemics in the upper Midwest of the U. S. have accounted for approximately 3 billion dollars in losses to U. S. agriculture due to low yields and price discounts due to toxin contaminated grain. Research in my laboratory has shown that both of these diseases are caused by several genetically distinct species that are non-indigenous to the United States. Our phylogenetic epidemiological studies are directed at minimizing the threat of inadvertent introductions of foreign FHB and SDS pathogens into the U. S. We are also using MLST to characterize the genetic diversity of medically important fusaria as part of a

multi-institution collaborative study. Lastly, some of my research has focused on the evolution of the Zygomycota and true morels (for publications, see below).

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## Selected Publications

### Evolution of *Fusarium* Head Blight (FHB) and trichothecene mycotoxins

**O'Donnell, K.**, Ward, T. J., Geiser, D. M., Kistler, H. C. and Aoki, T. 2004. Genealogical concordance between the mating type locus and seven other nuclear genes supports formal recognition of nine phylogenetically distinct species within the *Fusarium graminearum* clade. *Fungal Genetics and Biology* 41:600-623.

[Supplementary Materials](#)

Kimura, M., Tokai, T., **O'Donnell, K.**, Ward, T. J., Fujimura, M., Hamamoto, H., Shibata, T. and Yamaguchi, I. 2003. The trichothecene biosynthesis gene cluster of *Fusarium graminearum* F15 contains a limited number of essential pathway genes and expressed non-essential genes. *FEBS Letters* 539:105-110.

Ward, T. J., Bielawski, J. P., Kistler, H. C., Sullivan, E. and **O'Donnell, K.** 2002. Ancestral polymorphism and adaptive evolution in the trichothecene mycotoxin gene cluster of phytopathogenic *Fusarium*. *Proc. Natl. Acad. Sci. USA* 99:9278-9283.

**O'Donnell, K.**, Kistler, H.C., Tacke, B.K. and Casper, H.C. 2000. Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of *Fusarium graminearum*, the fungus causing wheat scab. *Proc. Natl. Acad. Sci. USA* 97:7905-7910.

**O'Donnell, K.**, Cigelnik, E. and Casper, H. H. 1998. Molecular phylogenetic, morphological, and mycotoxin data support reidentification of the Quorn mycoprotein fungus as *Fusarium venenatum*. *Fungal Genetics and Biology* 22:57-67.

### Evolution of the *Fusarium solani* species complex [including Sudden Death Syndrome (SDS) of soybean]

Aoki, T., **O'Donnell, K.**, Homma, Y. and Lattanzi, A. R. 2003. Sudden death syndrome of soybean is caused by two morphologically and phylogenetically distinct species within the *Fusarium solani* species complex, *F. virguliforme* in North America and *F. tucumaniae* in South America. *Mycologia* 95:660-684.

**O'Donnell, K.** 2000. Molecular phylogeny of the *Nectria haematococca* - *Fusarium solani* species complex. *Mycologia* 92:919-938.

### Evolution of the *Gibberella fujikuroi* species complex [mycotoxigenic phytopathogens, including most fumonisin producers]

Schweigkofler W, **O'Donnell K** and Garbelotto M. 2004. Detection and quantification of airborne conidia of *Fusarium circinatum*, the causal agent of pine pitch canker, from two California sites by using a real-time PCR approach combined with a simple spore trapping method. *Applied and Environmental Microbiology* 70:3512-3520.

**O'Donnell, K.**, Nirenberg, H.I., Aoki, T. and Cigelnik, E. 2000. A multigene phylogeny

of the *Gibberella fujikuroi* species complex: Detection of additional phylogenetically distinct species. *Mycoscience* 41:61-78.

**O'Donnell, K.**, Cigelnik, E. and Nirenberg, H. 1998. Molecular systematics and phylogeography of the *Gibberella fujikuroi* species complex. *Mycologia* 90:465-493

Nirenberg, H. and **O'Donnell, K.** 1998. New *Fusarium* species and combinations within the *Gibberella fujikuroi* species complex. *Mycologia* 90:434-458.

**O'Donnell, K.** and Cigelnik, E. 1997. Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. *Mol. Phylogenet. Evol.* 7:103-116.

Evolution of the *Fusarium oxysporum* species complex [wilt pathogens of many economically important plants]

**O'Donnell K.**, Sutton DA, Rinaldi MG, Magnon KC, Cox PA, Revankar SG, Sanche S, Geiser DM, Juba JH, van Burik JA, Padhye A, Anaissie EJ, Francesconi A, Walsh TJ, Robinson JS. 2004. Genetic diversity of human pathogenic members of the *Fusarium oxysporum* complex inferred from multilocus DNA sequence data and amplified fragment length polymorphism analyses: evidence for the recent dispersion of a geographically widespread clonal lineage and nosocomial origin. *Journal of Clinical Microbiology* 42:5109-5120.

Skovgaard, K., Nirenberg, H.I., **O'Donnell, K.** and Rosendahl, S. 2001. Evolution of *Fusarium oxysporum* f.sp. *vasinfectum* races inferred from multigene genealogies. *Phytopathology* 91:1231-1237.

Baayen, R.P., **O'Donnell, K.**, Breeuwsma, S., Geiser, D.M. and Waalwijk, C. 2001. Molecular relationships of fungi within the *Fusarium redolens*-*F. hostae* clade. *Phytopathology* 91:1037-1044.

Baayen, R.P., **O'Donnell, K.**, Waalwijk, C., Bonants, P.J.M., Cigelnik, E., Kroon, P. N. M. and Roebroek, E.J.A. 2000. Gene genealogies and AFLP analyses within the *Fusarium oxysporum* complex identify monophyletic and non-monophyletic formae speciales causing wilt and rot disease. *Phytopathology* 90:891-900.

**O'Donnell, K.**, Kistler, H.C., Cigelnik, E. and Ploetz, R.C. 1998. Multiple evolutionary origins of the fungus causing Panama disease of banana: Concordant evidence from nuclear and mitochondrial gene genealogies. *Proc. Natl. Acad. Sci. USA* 95:2044-2049.

Evolution of the Zygomycota

Taylor, T. W., Spatafora, J., **O'Donnell, K.**, Lutzoni, F., James, T., Hibbett, D. S., Geiser, D., Bruns, T. D. and Blackwell, M. 2003. The Kingdom Fungi. Assembling the Tree of Life. Yale University Press [In Press].

**O'Donnell, K.**, Lutzoni, F., Ward, T. J. and Benny G. L. 2001. Evolutionary relationships among mucoralean fungi (Zygomycota): Evidence for family polyphyly on a large scale. *Mycologia* 93:286-296.

Tanabe, Y., **O'Donnell, K.**, Saikawa, M. and Sugiyama, J. 2000. Molecular phylogeny of parasitic Zygomycota (Dimargaritales, Zoopagales) based on nuclear small subunit ribosomal DNA sequences. *Mol. Phylogenet. Evol.* 16:253-262.

Benny G.L. and **O'Donnell, K.** 2000. *Amoebidium parasiticum* is a protozoan, not a Trichomycete. *Mycologia* 92:1133-1137.

Voigt, K., Cigelnik, E. and **O'Donnell, K.** 1999. Phylogeny and PCR identification of clinically important Zygomycota based on nuclear rDNA sequence data. *J. Clin. Microbiol.* 37:3957-3964.

**O'Donnell, K.**, Cigelnik, E. and Benny G. L. 1998. Phylogenetic relationships among the Harpellales and Kickxellales. *Mycologia* 90:624-639.

#### Evolution of Morels and Truffles as well as other Ascomycota

Perez, J., Infante, F., Vega, F. E., Holguin, F., Macias, J., Valle, J., Nieto, G., **Peterson, S.W.**, Kurtzman, C.P., **O'Donnell, K.** 2003. Mycobiota associated with the coffee berry borer (*Hypothenemus hampei*) in Mexico. *Mycological Research* 107:879-887.

**O'Donnell, K.**, Cigelnik, E., Weber, N. S. and Trappe, J. M. 1997. Phylogenetic relationships among ascomycetous truffles and the true and false morels inferred from 18S and 28S ribosomal DNA sequence analysis. *Mycologia* 89:48-65.

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